Tacc3 Cas9-KO Strategy

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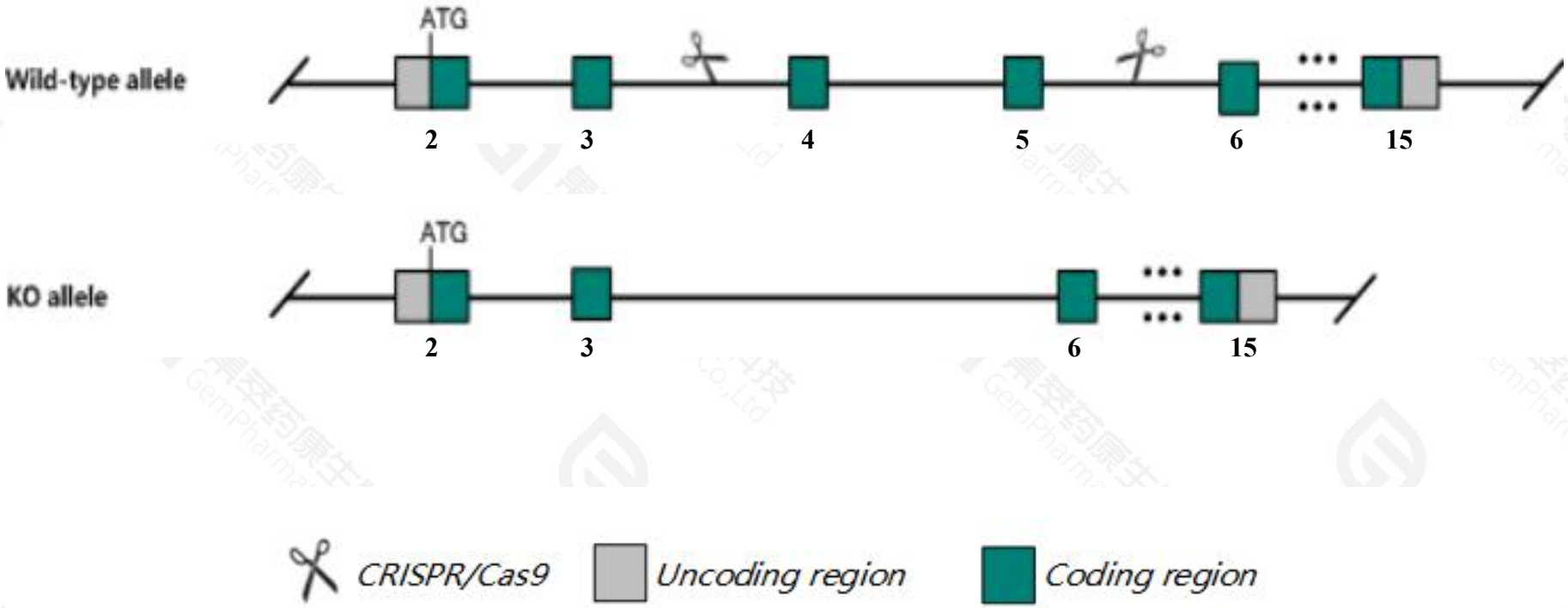
Project Overview

Project Name	***Tacc3***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tacc3* gene. The schematic diagram is as follows:



Technical routes

➢ The *Tacc3* gene has 8 transcripts. According to the structure of *Tacc3* gene, exon4-exon5 of *Tacc3-201*(ENSMUST00000074849.13) transcript is recommended as the knockout region.The region contains 671bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Tacc3* gene. The brief process is as follows: CRISPR/Cas9 system were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

Notice

➢ According to the existing MGI data,nullizygous mutations cause embryonic growth delay and prenatal death. Homozygotes for a null allele show hematopoietic deficiencies and severe facial clefts. Homozygotes for a hypomorphic allele die neonatally with malformed axial skeletons due to failed mitosis in mesenchymal sclerotome cells.

➢ The *Tacc3* gene is located on the Chr5. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes on the same chromosome.

➢ This strategy is designed based on genetic information in existing databases.Due to the complexity of biological processes,all risk of the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information （NCBI）

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Tacc3 transforming, acidic coiled-coil containing protein 3 [Mus musculus (house mouse)]

Gene ID: 21335, updated on 2-Mar-2021

Summary

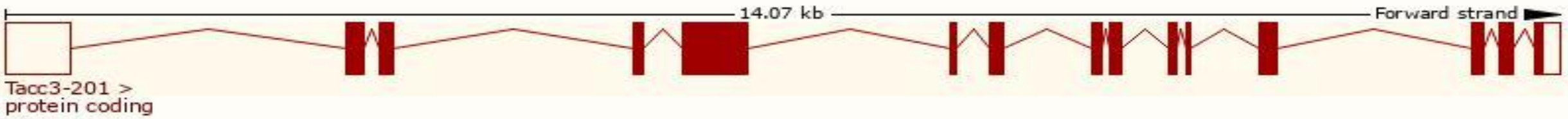
Official Symbol	Tacc3 provided by MGI
Official Full Name	transforming, acidic coiled-coil containing protein 3 provided byMGI
Primary source	MGI:MGI:1341163
See related	Ensembl:ENSMUSG00000037313
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	A, Aint, C86661, Eric1
Expression	Broad expression in CNS E11.5 (RPKM 34.6), liver E14 (RPKM 25.7) and 18 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

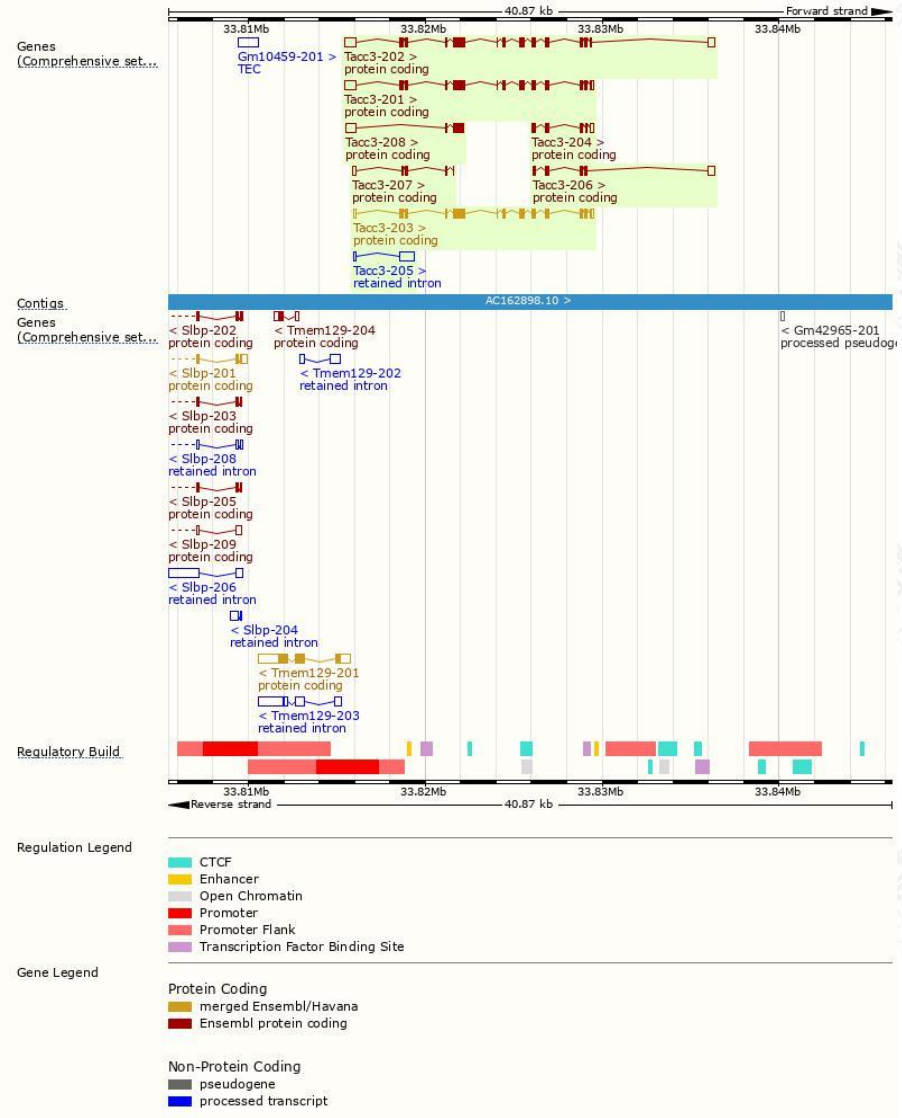
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tacc3-202	ENSMUST00000079534.11	2899	630aa	Protein coding	CCDS39065		TSL:1 , GENCODE basic , APPRIS P3 ,
Tacc3-201	ENSMUST00000074849.13	2669	637aa	Protein coding	CCDS80258		TSL:1 , GENCODE basic , APPRIS ALT2 ,
Tacc3-203	ENSMUST00000114426.10	2187	630aa	Protein coding	CCDS39065		TSL:1 , GENCODE basic , APPRIS P3 ,
Tacc3-208	ENSMUST00000201633.2	1242	206aa	Protein coding	-		CDS 3' incomplete , TSL:2 ,
Tacc3-206	ENSMUST00000139888.5	823	158aa	Protein coding	-		CDS 5' incomplete , TSL:3 ,
Tacc3-204	ENSMUST00000138240.5	679	136aa	Protein coding	-		CDS 5' incomplete , TSL:3 ,
Tacc3-207	ENSMUST00000152847.8	440	55aa	Protein coding	-		CDS 3' incomplete , TSL:3 ,
Tacc3-205	ENSMUST00000139453.2	888	No protein	Retained intron	-		TSL:1 ,

The strategy is based on the design of *Tacc3-201* transcript,the transcription is shown below:

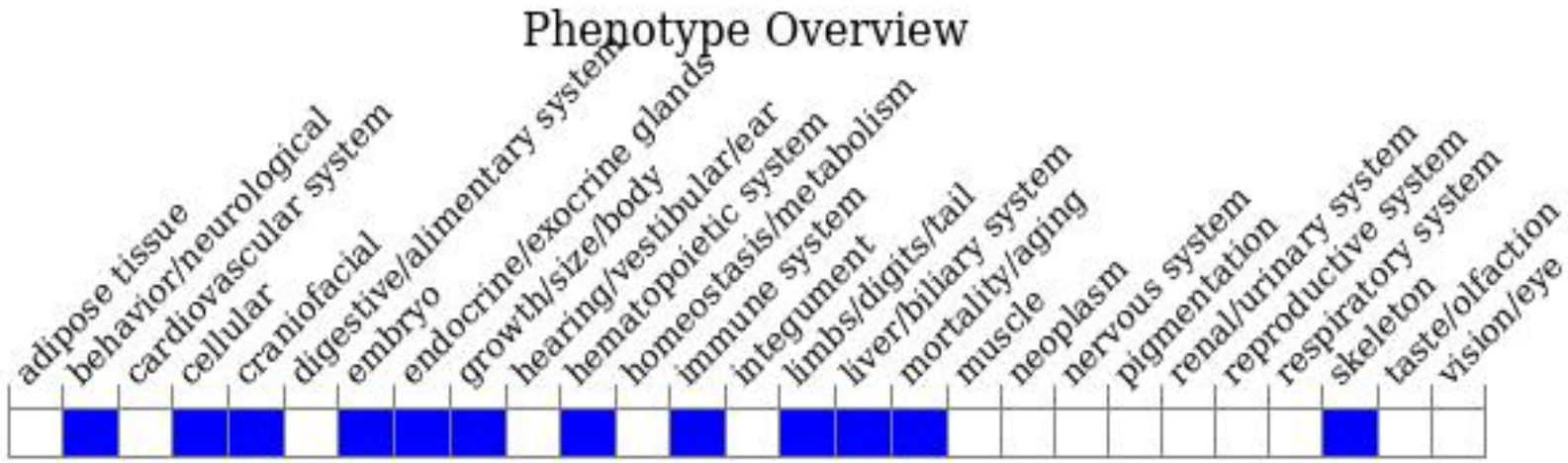


Genomic location distribution



Protein domain

Mouse phenotype description(MGI)



Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

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